

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/547,447

Source: pcr/10

Date Processed by STIC: 9/12/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 09/12/2005

PATENT APPLICATION: US/10/547,447

TIME: 13:37:01

Input Set : A:\12810-00119-US.txt

Output Set: N:\CRF4\09122005\J547447.raw

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3 <110> APPLICANT: Renz, Andreas
4      Heinz, Ernst
5      Abbadi, Amine
6      Domergue, Frederic
7      Zank, Thorsten
9 <120> TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF POLYUNSATURATED FATTY ACIDS
11 <130> FILE REFERENCE: 12810-00119-US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/547,447
C--> 13 <141> CURRENT FILING DATE: 2005-08-26
13 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/000771
14 <151> PRIOR FILING DATE: 2004-01-29
16 <150> PRIOR APPLICATION NUMBER: DE 103 08 836.9
17 <151> PRIOR FILING DATE: 2003-02-27
19 <160> NUMBER OF SEQ ID NOS: 57
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 849
25 <212> TYPE: DNA
26 <213> ORGANISM: Caenorhabditis elegans
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(849)
31 <223> OTHER INFORMATION: Acyl-CoA:lysophospholipid acyltransferase
34 <400> SEQUENCE: 1
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36 Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
37 1          5          10          15
39 ttc att tta tat aac ata tcg aca gta tgc cac tac tat atg cgg att      96
40 Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
41          20          25          30
43 tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt      144
44 Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
45          35          40          45
47 aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt      192
48 Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
49          50          55          60
51 cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc      240
52 His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
53 65          70          75          80
55 tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt      288
56 Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
57          85          90          95
59 aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg      336

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60 Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
61          100          105          110
63 aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc      384
64 Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
65          115          120          125
67 ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat      432
68 Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
69          130          135          140
71 aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg      480
72 Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
73 145          150          155          160
75 aag aac aga aat ctt aaa ctt tgg gta ttt ccg gaa gga aca aga aat      528
76 Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
77          165          170          175
79 cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca      576
80 Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
81          180          185          190
83 gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg      624
84 Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
85          195          200          205
87 gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt      672
88 Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
89          210          215          220
91 gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat      720
92 Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
93 225          230          235          240
95 gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc      768
96 Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
97          245          250          255
99 tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt      816
100 Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
101          260          265          270
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104 Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
105          275          280
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109 <211> LENGTH: 282
110 <212> TYPE: PRT
111 <213> ORGANISM: Caenorhabditis elegans
113 <400> SEQUENCE: 2
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116 1          5          10          15
119 Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
120          20          25          30
123 Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
124          35          40          45
127 Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
128          50          55          60
131 His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val

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132 65              70              75              80
135 Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
136              85              90              95
139 Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
140              100             105             110
143 Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
144              115             120             125
147 Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
148              130             135             140
151 Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
152 145             150             155             160
155 Lys Asn Arg Asn Leu Lys Leu Trp Val Phe Pro Glu Gly Thr Arg Asn
156              165             170             175
160 Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
161              180             185             190
164 Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
165              195             200             205
168 Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
169              210             215             220
172 Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
173 225             230             235             240
176 Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
177              245             250             255
180 Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
181              260             265             270
184 Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
185              275             280
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189 <211> LENGTH: 849
190 <212> TYPE: DNA
191 <213> ORGANISM: Caenorhabditis elegans
193 <220> FEATURE:
194 <221> NAME/KEY: CDS
195 <222> LOCATION: (1)..(849)
196 <223> OTHER INFORMATION: Acyl-CoA:lysophospholipid acyltransferase
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201 Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
202 1              5              10              15
204 ttc att tta tat aac ata tcg aca gta tgc cac tac tat atg cgg att      96
205 Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Met Arg Ile
206              20              25              30
208 tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt      144
209 Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
210              35              40              45
212 aca atg atc cct tct tgg cta aat ggg aag ggt gct gat tac gtg ttt      192
213 Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
214              50              55              60
216 cac tcg ttt ttc tat tgg tgt aaa tgg act ggt gtt cat aca aca gtc      240

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217 His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
218 65 70 75 80
220 tat gga tat gaa aaa aca caa gtt gaa ggt ccg gct gta gtt att tgt 288
221 Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
222 85 90 95
224 aat cat cag agt tct ctc gac att cta tcg atg gca tca atc tgg ccg 336
225 Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
226 100 105 110
228 aag aat tgt gtt gta atg atg aaa cga att ctt gcc tat gtt cca ttc 384
229 Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
230 115 120 125
232 ttc aat ctc gga gcc tac ttt tcc aac aca atc ttc atc gat cga tat 432
233 Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
234 130 135 140
236 aac cgt gaa cgt gcg atg gct tca gtt gat tat tgt gca tct gaa atg 480
237 Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
238 145 150 155 160
240 aag aac aga aat ctt aaa ctt tgg gta tct ccg gaa gga aca aga aat 528
241 Lys Asn Arg Asn Leu Lys Leu Trp Val Ser Pro Glu Gly Thr Arg Asn
242 165 170 175
244 cgt gaa gga ggg ttc att cca ttc aag aaa gga gca ttc aat att gca 576
245 Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
246 180 185 190
248 gtt cgt gcg cag att ccc att att cca gtt gta ttc tca gac tat cgg 624
249 Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
250 195 200 205
252 gat ttc tac tca aag cca ggc cga tat ttc aag aat gat gga gaa gtt 672
253 Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
254 210 215 220
256 gtt att cga gtt ctg gat gcg att cca aca aaa ggg ctc act ctt gat 720
257 Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
258 225 230 235 240
260 gac gtc agc gag ttg tct gat atg tgt cgg gac gtt atg ttg gca gcc 768
261 Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
262 245 250 255
264 tat aag gaa gtt act cta gaa gct cag caa cga aat gcg aca cgg cgt 816
265 Tyr Lys Glu Val Thr Leu Glu Ala Gln Gln Arg Asn Ala Thr Arg Arg
266 260 265 270
268 gga gaa aca aaa gac ggg aag aaa tct gag taa 849
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270 275 280
273 <210> SEQ ID NO: 4
274 <211> LENGTH: 282
275 <212> TYPE: PRT
276 <213> ORGANISM: Caenorhabditis elegans
278 <400> SEQUENCE: 4
280 Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
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285          20          25          30
288 Ser Phe Tyr Tyr Phe Thr Ile Leu Leu His Gly Met Glu Val Cys Val
289          35          40          45
292 Thr Met Ile Pro Ser Trp Leu Asn Gly Lys Gly Ala Asp Tyr Val Phe
293          50          55          60
296 His Ser Phe Phe Tyr Trp Cys Lys Trp Thr Gly Val His Thr Thr Val
297 65          70          75          80
300 Tyr Gly Tyr Glu Lys Thr Gln Val Glu Gly Pro Ala Val Val Ile Cys
301          85          90          95
304 Asn His Gln Ser Ser Leu Asp Ile Leu Ser Met Ala Ser Ile Trp Pro
305          100         105         110
308 Lys Asn Cys Val Val Met Met Lys Arg Ile Leu Ala Tyr Val Pro Phe
309          115         120         125
312 Phe Asn Leu Gly Ala Tyr Phe Ser Asn Thr Ile Phe Ile Asp Arg Tyr
313          130         135         140
316 Asn Arg Glu Arg Ala Met Ala Ser Val Asp Tyr Cys Ala Ser Glu Met
317 145          150          155          160
320 Lys Asn Arg Asn Leu Lys Leu Trp Val Ser Pro Glu Gly Thr Arg Asn
321          165         170         175
324 Arg Glu Gly Gly Phe Ile Pro Phe Lys Lys Gly Ala Phe Asn Ile Ala
325          180         185         190
328 Val Arg Ala Gln Ile Pro Ile Ile Pro Val Val Phe Ser Asp Tyr Arg
329          195         200         205
332 Asp Phe Tyr Ser Lys Pro Gly Arg Tyr Phe Lys Asn Asp Gly Glu Val
333          210         215         220
336 Val Ile Arg Val Leu Asp Ala Ile Pro Thr Lys Gly Leu Thr Leu Asp
337 225         230         235         240
340 Asp Val Ser Glu Leu Ser Asp Met Cys Arg Asp Val Met Leu Ala Ala
341          245         250         255
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345          260         265         270
348 Gly Glu Thr Lys Asp Gly Lys Lys Ser Glu
349          275         280
352 <210> SEQ ID NO: 5
353 <211> LENGTH: 849
354 <212> TYPE: DNA
355 <213> ORGANISM: Caenorhabditis elegans
357 <220> FEATURE:
358 <221> NAME/KEY: CDS
359 <222> LOCATION: (1)..(849)
360 <223> OTHER INFORMATION: Acyl-CoA:lysophospholipid acyltransferase
363 <400> SEQUENCE: 5
364 atg gag aac ttc tgg tcg atc gtc gtg ttt ttt cta ctc tca att ctc      48
365 Met Glu Asn Phe Trp Ser Ile Val Val Phe Phe Leu Leu Ser Ile Leu
366 1          5          10          15
368 ttc att tta tat aac ata tcg aca gta tgc cac tac tat gtg cgg att      96
369 Phe Ile Leu Tyr Asn Ile Ser Thr Val Cys His Tyr Tyr Val Arg Ile
370          20          25          30
372 tcg ttt tat tac ttc aca att tta ttg cat gga atg gaa gtt tgt gtt      144

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 09/12/2005

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Input Set : A:\12810-00119-US.txt

Output Set: N:\CRF4\09122005\J547447.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:15; Line(s) 1417
Seq#:16; Line(s) 1552
Seq#:17; Line(s) 1686
Seq#:18; Line(s) 1820
Seq#:26; Line(s) 3220
Seq#:27; Line(s) 3417
Seq#:30; Line(s) 4671
Seq#:31; Line(s) 5117

VERIFICATION SUMMARY

DATE: 09/12/2005

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Input Set : A:\12810-00119-US.txt

Output Set: N:\CRF4\09122005\J547447.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date